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<110> ADLER, JON ELLIOT
LI, XIAODONG
STASZEWSKI, LENA
O'CONNELL, SHAWN
ZOZULYA, SERGEY

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<170> PatentIn Ver. 2.1

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 Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
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 Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
 65 70 75 80

Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
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Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
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Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
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Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
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His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
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Leu Met Pro Gln Val Ser Tyr Gly Ala Ser Met Glu Leu Leu Ser Ala
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Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr Val Pro Ser Asp Arg Val
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Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln Glu Phe Gly Trp Asn Trp
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Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr Gly Arg Gln Gly Leu Ser
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Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly Ile Cys Ile Ala His Glu
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Gly Leu Val Pro Leu Pro Arg Ala Asp Asp Ser Arg Leu Gly Lys Val
 245 250 255

Gln Asp Val Leu His Gln Val Asn Gln Ser Ser Val Gln Val Val Leu
 260 265 270

Leu Phe Ala Ser Val His Ala Ala His Ala Leu Phe Asn Tyr Ser Ile
 275 280 285

Ser Ser Arg Leu Ser Pro Lys Val Trp Val Ala Ser Glu Ala Trp Leu
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Thr Ser Asp Leu Val Met Gly Leu Pro Gly Met Ala Gln Met Gly Thr
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Val Leu Gly Phe Leu Gln Arg Gly Ala Gln Leu His Glu Phe Pro Gln
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Tyr Val Lys Thr His Leu Ala Leu Ala Thr Asp Pro Ala Phe Cys Ser
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Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu Glu Asp Val Val Gly Gln
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Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu Gln Asn Val Ser Ala Gly
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Leu Asn His His Gln Thr Phe Ser Val Tyr Ala Ala Val Tyr Ser Val
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Ala Gln Ala Leu His Asn Thr Leu Gln Cys Asn Ala Ser Gly Cys Pro
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Ala Gln Asp Pro Val Lys Pro Trp Gln Leu Leu Glu Asn Met Tyr Asn
420 425 430

Leu Thr Phe His Val Gly Gly Leu Pro Leu Arg Phe Asp Ser Ser Gly
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Asn Val Asp Met Glu Tyr Asp Leu Lys Leu Trp Val Trp Gln Gly Ser
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Val Pro Arg Leu His Asp Val Gly Arg Phe Asn Gly Ser Leu Arg Thr
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Glu Arg Leu Lys Ile Arg Trp His Thr Ser Asp Asn Gln Lys Pro Val
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Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly Gln Val Arg Arg Val Lys
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Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys Thr Phe Cys Gly Gln Asp
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Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys Phe Arg Arg Arg Ser Arg
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Ser Leu Ala Leu Gly Leu Val Leu Ala Ala Leu Gly Leu Phe Val His
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His Arg Asp Ser Pro Leu Val Gln Ala Ser Gly Gly Pro Leu Ala Cys
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Phe Gly Leu Val Cys Leu Gly Leu Val Cys Leu Ser Val Leu Leu Phe
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Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu Ala Gln Gln Pro Leu Ser
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His Leu Pro Leu Thr Gly Cys Leu Ser Thr Leu Phe Leu Gln Ala Ala
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Glu Ile Phe Val Glu Ser Glu Leu Pro Leu Ser Trp Ala Asp Arg Leu
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Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp Leu Val Val Leu Leu Ala
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Cys	Leu	Ala	Gln	Gln	Pro	Met	Ala	His	Leu	Pro	Leu	Thr	Gly	Cys	Leu
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Pro	Leu	Ser	Trp	Ala	Asn	Trp	Leu	Cys	Ser	Tyr	Leu	Arg	Asp	Ser	Gly
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Pro	Thr	Glu	Val	Leu	Glu	His	Cys	His	Val	Arg	Ser	Trp	Val	Asn	Leu
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Phe Cys Leu Ser Val Leu Leu Phe Pro Gly Arg Pro Arg Ser Ala Ser
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Cys Leu Ala Gln Gln Pro Met Ala His Leu Pro Leu Thr Gly Cys Leu
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Ser Thr Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu
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Pro Leu Ser Trp Ala Asn Trp Leu Cys Ser Tyr Leu Arg Gly Pro Trp
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Ala Trp Leu Val Val Leu Leu Ala Thr Leu Val Glu Ala Ala Leu Cys
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Ala Trp Tyr Leu Met Ala Phe Pro Pro Glu Val Val Thr Asp Trp Gln
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 Cys Cys Trp Ala Phe Ala Cys His Ser Thr Glu Ser Ser Pro Asp Phe
 20 25 30
 Thr Leu Pro Gly Asp Tyr Leu Leu Ala Gly Leu Phe Pro Leu His Ser
 35 40 45
 Gly Cys Leu Gln Val Arg His Arg Pro Glu Val Thr Leu Cys Asp Arg
 50 55 60
 Ser Cys Ser Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg
 65 70 75 80
 Leu Gly Val Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile
 85 90 95
 Thr Leu Gly Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val
 100 105 110

Tyr Ala Thr Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu
 115 120 125

Leu Gln Gly Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile
 130 135 140

Gly Pro Asp Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser
 145 150 155 160

Pro Phe Leu Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu
 165 170 175

Ser Val Lys Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp
 180 185 190

Lys Tyr Gln Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp
 195 200 205

Thr Trp Ile Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly
 210 215 220

Val Gln Ala Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala
 225 230 235 240

Phe Lys Asp Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met
 245 250 255

Gln Cys Leu Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val
 260 265 270

Val Phe Ser Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val
 275 280 285

Leu Thr Asn Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala
 290 295 300

Leu Ser Arg His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met
 305 310 315 320

Val Leu Gly Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala
 325 330 335

Phe Glu Glu Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys
 340 345 350

His Lys Gly Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln
 355 360 365

Ala Phe Met Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser
 370 375 380

Ser Ala Tyr Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu
 385 390 395 400

His Gln Leu Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val
 405 410 415

Tyr Pro Trp Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu
 420 425 430

His Lys Asp Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser
 435 440 445

Tyr Asn Ile Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr
 450 455 460

Val Leu Gly Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu
 465 470 475 480

Thr Lys Ile Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val
 485 490 495

Cys Ser Ser Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe
 500 505 510

His His Cys Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu
 515 520 525

Asn Lys Ser Asp Leu Tyr Arg Cys Gln Pro Cys Gly Lys Glu Glu Trp
 530 535 540

Ala Pro Glu Gly Ser Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu
 545 550 555 560

Ala Leu Arg Glu His Thr Ser Trp Val Leu Leu Ala Ala Asn Thr Leu
 565 570 575

Leu Leu Leu Leu Leu Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu
 580 585 590

Asp Thr Pro Val Val Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met
 595 600 605

Leu Gly Ser Leu Ala Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly
 610 615 620

Glu Pro Thr Arg Pro Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu
 625 630 635 640

Gly Phe Thr Ile Phe Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu
 645 650 655

Ile Ile Ile Phe Lys Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala
 660 665 670

Trp Val Gln Asn His Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala
 675 680 685

Ala Gln Leu Leu Ile Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu
 690 695 700

Pro Ala Arg Glu Tyr Gln Arg Phe Pro His Leu Val Met Leu Glu Cys
 705 710 715 720

Thr Glu Thr Asn Ser Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly
 725 730 735

Leu Leu Ser Ile Ser Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu
 740 745 750

Pro Glu Asn Tyr Asn Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe
 755 760 765

Asn Phe Val Ser Trp Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp
 770 775 780

Gly Lys Tyr Leu Pro Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu
 785 790 795 800

Ser Ser Gly Phe Gly Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu
 805 810 815

Cys Arg Pro Asp Leu Asn Ser Thr Glu His Phe Gln Ala Ser Ile Gln
 820 825 830

Asp Tyr Thr Arg Arg Cys Gly Ser Thr
 835 840

<210> 18

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
sequence

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<221> MOD_RES

<222> (1)

<223> Thr or Arg

<220>

<221> MOD_RES

<222> (3)

<223> Phe or Leu

<220>

<221> MOD_RES

<222> (4)

<223> Arg, Gln or Pro

<220>

<221> MOD_RES

<222> (6)

<223> Arg or Thr

<220>

<221> MOD_RES

<222> (7)

<223> Ser, Pro or Val

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<220>
<221> MOD_RES
<222> (8)
<223> Val, Glu, Arg, Lys or Thr

<220>
<221> MOD_RES
<222> (11)
<223> Ala or Glu

<220>
<221> MOD_RES
<222> (12)
<223> Trp or Leu

<220>
<221> MOD_RES
<222> (13)
<223> Arg, His or Gly

<400> 18
Xaa Cys Xaa Xaa Arg Xaa Xaa Xaa Phe Leu Xaa Xaa Xaa Glu
      1           5           10

<210> 19
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
      sequence

<220>
<221> MOD_RES
<222> (1)
<223> Leu or Gln

<220>
<221> MOD_RES
<222> (3)
<223> Glu, Gly or Thr

<220>
<221> MOD_RES
<222> (4)
<223> Asn, Arg or Cys

<220>
<221> MOD_RES
<222> (7)
<223> Arg or Glu

<220>
<221> MOD_RES
<222> (9)
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<223> Arg or Lys

<220>
<221> MOD_RES
<222> (10)
<223> Cys, Gly or Phe

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<220>
<221> MOD_RES
<222> (11)
<223> Val, Leu or Ile
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<220>
<221> MOD_RES
<222> (13)
<223> Phe or Leu

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<220>
<221> MOD_RES
<222> (14)
<223> Ala or Ser
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<220>
<221> MOD_RES
<222> (15)
<223> Met or Leu

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<210> 20
<211> 3563
<212> DNA
<213> Homo sapiens
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 acgtggacac ccctgtgacc atc 3563

<210> 21
 <211> 839
 <212> PRT
 <213> Homo sapiens

<400> 21
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 Val Leu Ala Glu Pro Ala Glu Asn Ser Asp Phe Tyr Leu Pro Gly Asp
 20 25 30
 Tyr Leu Leu Gly Gly Leu Phe Ser Leu His Ala Asn Met Lys Gly Ile
 35 40 45

Val His Leu Asn Phe Leu Gln Val Pro Met Cys Lys Glu Tyr Glu Val
 50 55 60

Lys Val Ile Gly Tyr Asn Leu Met Gln Ala Met Arg Phe Ala Val Glu
 65 70 75 80

Glu Ile Asn Asn Asp Ser Ser Leu Leu Pro Gly Val Leu Leu Gly Tyr
 85 90 95

Glu Ile Val Asp Val Cys Tyr Ile Ser Asn Asn Val Gln Pro Val Leu
 100 105 110

Tyr Phe Leu Ala His Glu Asp Asn Leu Leu Pro Ile Gln Glu Asp Tyr
 115 120 125

Ser Asn Tyr Ile Ser Arg Val Val Ala Val Ile Gly Pro Asp Asn Ser
 130 135 140

Glu Ser Val Met Thr Val Ala Asn Phe Leu Ser Leu Phe Leu Leu Pro
 145 150 155 160

Gln Ile Thr Tyr Ser Ala Ile Ser Asp Glu Leu Arg Asp Lys Val Arg
 165 170 175

Phe Pro Ala Leu Leu Arg Thr Thr Pro Ser Ala Asp His His Val Glu
 180 185 190

Ala Met Val Gln Leu Met Leu His Phe Arg Trp Asn Trp Ile Ile Val
 195 200 205

Leu Val Ser Ser Asp Thr Tyr Gly Arg Asp Asn Gly Gln Leu Leu Gly
 210 215 220

Glu Arg Val Ala Arg Arg Asp Ile Cys Ile Ala Phe Gln Glu Thr Leu
 225 230 235 240

Pro Thr Leu Gln Pro Asn Gln Asn Met Thr Ser Glu Glu Arg Gln Arg
 245 250 255

Leu Val Thr Ile Val Asp Lys Leu Gln Gln Ser Thr Ala Arg Val Val
 260 265 270

Val Val Phe Ser Pro Asp Leu Thr Leu Tyr His Phe Phe Asn Glu Val
 275 280 285

Leu Arg Gln Asn Phe Thr Gly Ala Val Trp Ile Ala Ser Glu Ser Trp
 290 295 300

Ala Ile Asp Pro Val Leu His Asn Leu Thr Glu Leu Gly His Leu Gly
 305 310 315 320

Thr Phe Leu Gly Ile Thr Ile Gln Ser Val Pro Ile Pro Gly Phe Ser
 325 330 335

Glu Phe Arg Glu Trp Gly Pro Gln Ala Gly Pro Pro Pro Leu Ser Arg
 340 345 350

Thr Ser Gln Ser Tyr Thr Cys Asn Gln Glu Cys Asp Asn Cys Leu Asn
 355 360 365

Ala Thr Leu Ser Phe Asn Thr Ile Leu Arg Leu Ser Gly Glu Arg Val
 370 375 380

Val Tyr Ser Val Tyr Ser Ala Val Tyr Ala Val Ala His Ala Leu His
 385 390 395 400

Ser Leu Leu Gly Cys Asp Lys Ser Thr Cys Thr Lys Arg Val Val Tyr
 405 410 415

Pro Trp Gln Leu Leu Glu Glu Ile Trp Lys Val Asn Phe Thr Leu Leu
 420 425 430

Asp His Gln Ile Phe Phe Asp Pro Gln Gly Asp Val Ala Leu His Leu
 435 440 445

Glu Ile Val Gln Trp Gln Trp Asp Arg Ser Gln Asn Pro Phe Gln Ser
 450 455 460

Val Ala Ser Tyr Tyr Pro Leu Gln Arg Gln Leu Lys Asn Ile Gln Asp
 465 470 475 480

Ile Ser Trp His Thr Val Asn Asn Thr Ile Pro Met Ser Met Cys Ser
 485 490 495

Lys Arg Cys Gln Ser Gly Gln Lys Lys Lys Pro Val Gly Ile His Val
 500 505 510

Cys Cys Phe Glu Cys Ile Asp Cys Leu Pro Gly Thr Phe Leu Asn His
 515 520 525

Thr Glu Asp Glu Tyr Glu Cys Gln Ala Cys Pro Asn Asn Glu Trp Ser
 530 535 540

Tyr Gln Ser Glu Thr Ser Cys Phe Lys Arg Gln Leu Val Phe Leu Glu
 545 550 555 560

Trp His Glu Ala Pro Thr Ile Ala Val Ala Leu Leu Ala Ala Leu Gly
 565 570 575

Phe Leu Ser Thr Leu Ala Ile Leu Val Ile Phe Trp Arg His Phe Gln
 580 585 590

Thr Pro Ile Val Arg Ser Ala Gly Gly Pro Met Cys Phe Leu Met Leu
 595 600 605

Thr Leu Leu Leu Val Ala Tyr Met Val Val Pro Val Tyr Val Gly Pro
 610 615 620

Pro Lys Val Ser Thr Cys Leu Cys Arg Gln Ala Leu Phe Pro Leu Cys
 625 630 635 640

Phe Thr Ile Cys Ile Ser Cys Ile Ala Val Arg Ser Phe Gln Ile Val
 645 650 655

Cys Ala Phe Lys Met Ala Ser Arg Phe Pro Arg Ala Tyr Ser Tyr Trp
 660 665 670
 Val Arg Tyr Gln Gly Pro Tyr Val Ser Met Ala Phe Ile Thr Val Leu
 675 680 685
 Lys Met Val Ile Val Val Ile Gly Met Leu Ala Thr Gly Leu Ser Pro
 690 695 700
 Thr Thr Arg Thr Asp Pro Asp Asp Pro Lys Ile Thr Ile Val Ser Cys
 705 710 715 720
 Asn Pro Asn Tyr Arg Asn Ser Leu Leu Phe Asn Thr Ser Leu Asp Leu
 725 730 735
 Leu Leu Ser Val Val Gly Phe Ser Phe Ala Tyr Met Gly Lys Glu Leu
 740 745 750
 Pro Thr Asn Tyr Asn Glu Ala Lys Phe Ile Thr Leu Ser Met Thr Phe
 755 760 765
 Tyr Phe Thr Ser Ser Val Ser Leu Cys Thr Phe Met Ser Ala Tyr Ser
 770 775 780
 Gly Val Leu Val Thr Ile Val Asp Leu Leu Val Thr Val Leu Asn Leu
 785 790 795 800
 Leu Ala Ile Ser Leu Gly Tyr Phe Gly Pro Lys Cys Tyr Met Ile Leu
 805 810 815
 Phe Tyr Pro Glu Arg Asn Thr Pro Ala Tyr Phe Asn Ser Met Ile Gln
 820 825 830
 Gly Tyr Thr Met Arg Arg Asp
 835

<210> 22
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 PDZIP peptide sequence

<400> 22
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<210> 23
 <211> 2520
 <212> DNA
 <213> Homo sapiens

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<210> 24
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Six-His tag

<400> 24
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